

In re Application No.: 09/580,491  
Attorney Docket No. 07691.0009

A1  
cont

mutational patterns that have been observed and reported for HIV-1 and that are correlated with drug resistance are very diverse: some antiretroviral agents require only one single genetic change, while others require multiple mutations for resistance to appear. A summary of mutations in the HIV genome correlated with drug resistance has been compiled. See Schinazi, R.F., Larder, B.A. & Meliors, J.W. 1997. Int. Antiviral News 5, 129-142 (1997). Additionally, an electronic listing with mutations has also become available on the internet at sites such as hiv-web.lanl.gov or www.viralresistance.com. - -

On Page 24, please replace Table 2b with the following table:

**Table 2b: Novel Protease Mutations and the Correlated Drug Resistance**

A2

Protease Mutation	Resistant to:
33F + 90M	PI
88T	PI

**IN THE CLAIMS**

Please amend claim 7 as follows:

7. (Amended) A method of evaluating the effectiveness of an antiviral therapy of an HIV-infected patient comprising:

(i) collecting a sample from an HIV-infected patient;

(ii) determining whether the sample comprises at least one nucleic acid chosen from:

(a) a first nucleic acid encoding HIV reverse transcriptase comprising at least one mutation chosen from:

1) at least one mutation chosen from 88E, 101H, 101N, 101P, 101Q, 101T, 103H, 103S, 179I, 179E, 181V, 190E, 190S, and 190T,

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2) mutations 103 R and 179D, or

3) combinations of 1) and 2),

in which the presence of said at least one mutation correlates with resistance to at least one Non-Nucleoside Reverse Transcriptase Inhibitor (NNRTI);

(b) a second nucleic acid encoding HIV reverse transcriptase comprising at least one mutation chosen from 69S-[S-S], 184G, 184L, 215 V, 44D, 44A, and 118I,

in which the presence of said at least one mutation correlates with resistance to at least one Nucleoside Reverse Transcriptase Inhibitor (NRTI); and

(c) a third nucleic acid encoding HIV protease comprising at least one mutation chosen from:

1) 88T,

2) mutations 33F and 90M, or

3) combinations of 1) and 2),

in which the presence of said at least one mutation correlates with resistance to at least one Protease Inhibitor (PI); and

(iii) using the presence of said at least one nucleic acid to evaluate the effectiveness of said antiviral therapy.

#### REMARKS

Claims 1-30 are pending in this application. Claim 7 has been amended to clarify claim language and to replace abbreviations. The scope of claim 7 has not been narrowed by these amendments.